



results of BLAST

BLASTN 2.2.9 [May-01-2004]

RID: 1095189908-5183-132949771792.BLASTQ4

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
2,595,971 sequences; 11,738,793,097 total letters

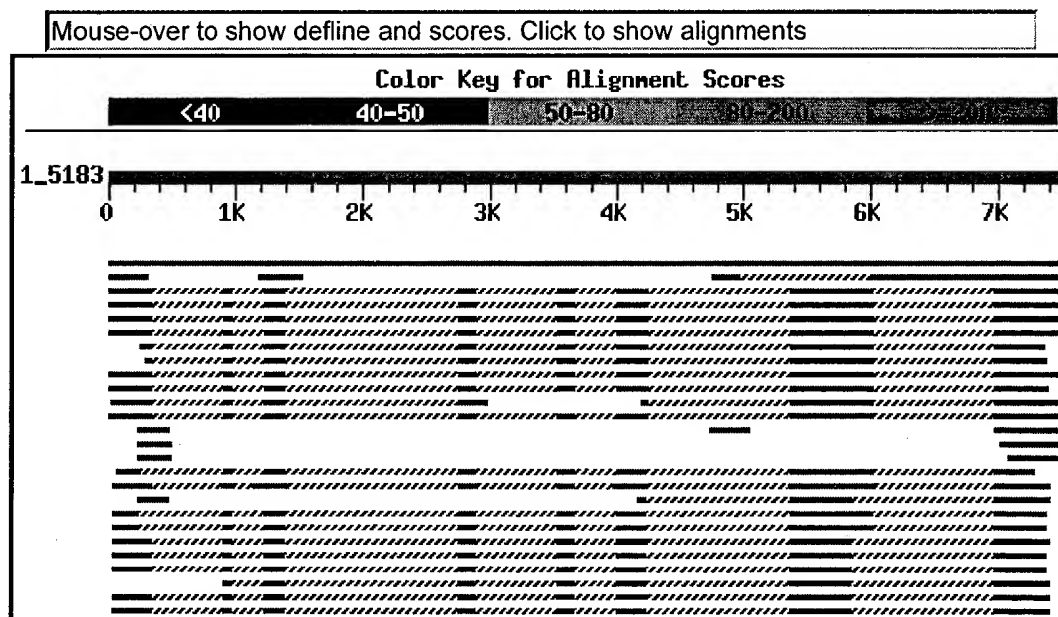
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Query=

(7491 letters)

Distribution of 4588 Blast Hits on the Query Sequence



Sequences producing significant alignments:

	Score	E	
	(bits)	Value	
gi 13270751 gb AC013439.11 Homo sapiens BAC clone RP11-270...	4556	0.0	
gi 31873559 emb BX537503.1 HSM805934 Homo sapiens mRNA; cDN...	2258	0.0	U
gi 31543639 ref NM_014585.3 Homo sapiens solute carrier fa...	1243	0.0	UE
gi 22902429 gb BC037733.1 Homo sapiens solute carrier fami...	1243	0.0	UE
gi 7109248 gb AF226614.1 AF226614 Homo sapiens ferroportin1...	1243	0.0	U

gi 50499943 emb CR619136.1	full-length cDNA clone CS0DI006...	1243	0.0	U
gi 12053382 emb AL136944.1 HSM801908	Homo sapiens mRNA; cDN...	1243	0.0	UE
gi 49065553 emb CR533564.1	Homo sapiens full open reading ...	1243	0.0	U
gi 23273531 gb BC035893.1	Homo sapiens solute carrier fami...	1237	0.0	UE
gi 7264728 gb AF231121.1 AF231121	Homo sapiens iron-regulat...	1237	0.0	U
gi 7023677 dbj AK002038.1	Homo sapiens cDNA FLJ11176 fis, ...	1221	0.0	U
gi 8895484 gb AF215636.1 AF215636	Homo sapiens SLC11A3 iron...	1219	0.0	U
gi 4761673 gb AF147322.1 AF147322	Homo sapiens full length ...	987	0.0	U
gi 50479265 emb CR598458.1	full-length cDNA clone CS0DI015...	896	0.0	U
gi 50487448 emb CR606641.1	full-length cDNA clone CS0DI060...	794	0.0	U
gi 18846873 gb AF394785.3	Rattus norvegicus ferroportin 1 ...	681	0.0	U
gi 28933915 gb AC123557.4	Mus musculus BAC clone RP23-183P...	668	0.0	
gi 40204822 emb AJ616848.1	Homo sapiens partial SLC40A1 ge...	660	0.0	
gi 26328524 dbj AK032732.1	Mus musculus 12 days embryo mal...	652	0.0	U
gi 18959259 ref NM 133315.1	Rattus norvegicus solute carri...	650	0.0	UE
gi 4098298 gb U76714.1 RRU76714	Rattus norvegicus cell adhe...	650	0.0	UE
gi 13097389 gb BC003438.1	Mus musculus solute carrier fami...	646	0.0	UE
gi 7109246 gb AF226613.1 AF226613	Mus musculus ferroportin1...	646	0.0	U
gi 12843053 dbj AK008700.1	Mus musculus adult male stomach...	646	0.0	UE
gi 8895486 gb AF215637.1 AF215637	Mus musculus SLC11A3 iron...	646	0.0	U
gi 8394303 ref NM 016917.1	Mus musculus solute carrier fam...	644	0.0	UE
gi 7264726 gb AF231120.1 AF231120	Mus musculus iron-regulat...	644	0.0	UE
gi 38043879 emb AJ604512.1	Homo sapiens partial SLC40A1 ge...	610	e-170	
gi 33337961 gb AF171087.1	Homo sapiens MSTP079 (MST079) mR...	593	e-165	U
gi 1028149 emb Z56918.1 HS153B8F	H.sapiens CpG island DNA g...	496	e-136	
gi 1028150 emb Z56919.1 HS153B8R	H.sapiens CpG island DNA g...	496	e-136	
gi 1028147 emb Z56916.1 HS153B7F	H.sapiens CpG island DNA g...	487	e-133	
gi 1028148 emb Z56917.1 HS153B7R	H.sapiens CpG island DNA g...	481	e-131	
gi 22657470 gb AC130004.4	Homo sapiens 3 BAC RP11-237K2 (R...	469	e-128	
gi 4056509 gb AC005815.1	Homo sapiens chromosome 22 clone ...	468	e-127	
gi 14018263 emb AL355794.5	Human DNA sequence from clone R...	468	e-127	
gi 18476535 emb AL160278.24	Human DNA sequence from clone ...	468	e-127	
gi 19848493 gb AC073344.7	Homo sapiens BAC clone RP11-628B...	466	e-127	
gi 14522995 gb AC087729.2	Pan troglodytes clone RP43-143F1...	466	e-127	
gi 29294416 gb AC142297.1	Pan troglodytes BAC clone RP43-9...	466	e-127	
gi 13794592 dbj AP003357.2	Homo sapiens genomic DNA, chrom...	464	e-126	E
gi 2695811 emb AL008709.1 HS262B17	Human DNA sequence from ...	464	e-126	
gi 16972823 emb AL162590.15	Human DNA sequence from clone ...	464	e-126	
gi 29294468 gb AC142349.1	Pan troglodytes BAC clone RP43-9...	464	e-126	
gi 13899438 gb AC006435.7 AC006435	Homo sapiens chromosome ...	464	e-126	
gi 12232486 gb AC023471.4 AC023471	Homo sapiens chromosome ...	462	e-126	
gi 12007690 gb AC018818.5 AC018818	Homo sapiens chromosome ...	462	e-126	
gi 3242763 gb AC005154.1	Homo sapiens PAC clone RP4-777023...	462	e-126	E
gi 15668116 gb AC019051.8	Homo sapiens BAC clone RP11-92L2...	462	e-126	
gi 14245761 dbj AP002371.3	Homo sapiens genomic DNA, chrom...	460	e-125	
gi 3645947 gb AC002543.1	Homo sapiens BAC clone CTA-300C3 ...	460	e-125	E
gi 13235049 emb AL132777.4 CNS01DTI	Human chromosome 14 DNA...	460	e-125	
gi 14196410 gb AC013264.4	Homo sapiens BAC clone RP11-184N...	460	e-125	
gi 20377033 gb AC103691.2	Homo sapiens chromosome 15, clon...	458	e-125	
gi 19774295 gb AC092962.4	Homo sapiens 3 BAC RP11-698E5 (R...	458	e-125	
gi 19774525 gb AC095034.2	Homo sapiens chromosome 1 clone ...	458	e-125	
gi 15145609 gb AC016758.7	Homo sapiens BAC clone RP11-535E...	458	e-125	

gi 18093148 gb AC012365.6 	Homo sapiens BAC clone RP11-459C...	458	e-125
gi 15487468 gb AC023122.9 	Homo sapiens BAC clone RP11-297L...	458	e-125
gi 17939960 dbj AP003119.2 	Homo sapiens genomic DNA, chrom...	458	e-125
gi 17939959 dbj AP003101.2 	Homo sapiens genomic DNA, chrom...	458	e-125
gi 15706138 gb AC018574.6 	Homo sapiens chromosome , clone ...	458	e-125
gi 14141748 gb AC012377.5 AC012377	Homo sapiens chromosome ...	458	e-125
gi 3859654 gb AC005863.1 AC005863	Homo sapiens chromosome 1...	458	e-125
gi 12658001 gb AC023908.6 AC023908	Homo sapiens chromosome ...	458	e-125
gi 16304939 emb AL442123.12 	Human DNA sequence from clone ...	458	e-125
gi 21747443 gb AC011495.8 	Homo sapiens chromosome 19 clone...	458	e-125
gi 21240682 gb AC010619.7 	Homo sapiens chromosome 19 clone...	458	e-125
gi 11544981 emb AL354857.13 	Human DNA sequence from clone ...	458	e-125
gi 19698714 gb AC024337.8 	Homo sapiens chromosome 15, clon...	458	e-125
gi 19549309 gb AC079209.6 	Homo sapiens chromosome 8, clone...	458	e-125
gi 25815260 gb AC135893.2 	Homo sapiens 3 BAC RP11-643E20 (...)	458	e-125
gi 9581599 emb AL162458.10 	Human DNA sequence from clone R...	458	e-125 E
gi 11228434 emb AL450226.1 HSBC17A99	Homo sapiens chromosom...	458	e-125
gi 11228433 emb AL450224.1 HSBC17A96	Homo sapiens chromosom...	458	e-125
gi 7330682 emb AL121903.13 HSDJ155G6	Human DNA sequence fro...	458	e-125
gi 24308594 gb AC122692.4 	Homo sapiens X BAC RP13-675A2 (R...	456	e-124
gi 23322827 gb AC128673.4 	Homo sapiens BAC clone RP11-1195...	456	e-124
gi 21747464 gb AC092329.3 	Homo sapiens chromosome 19 clone...	456	e-124
gi 28625947 gb AF490843.1 	Homo sapiens clone PAC 70L19, HO...	456	e-124
gi 28460736 gb AC023794.37 	Homo sapiens 12 BAC RP11-834C11...	456	e-124
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gi 16356871 gb AC025175.4 	Homo sapiens chromosome 5 clone ...	456	e-124
gi 15375163 gb AC026779.5 	Homo sapiens chromosome 5 clone ...	456	e-124
gi 11094680 gb AC010165.10 AC010165	Homo sapiens chromosome...	456	e-124
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gi 7262575 dbj AP001256.2 	Homo sapiens genomic DNA, chromo...	456	e-124
gi 12025651 gb AC013470.10 	Homo sapiens BAC clone RP11-472...	454	e-123
gi 29788915 gb AC111182.20 	Homo sapiens chromosome 17, clo...	454	e-123
gi 20279414 gb AC116334.2 	Homo sapiens chromosome 5 clone ...	454	e-123
gi 31790744 dbj AP000904.6 	Homo sapiens genomic DNA, chrom...	454	e-123
gi 16974294 gb AC017116.7 	Homo sapiens BAC clone CTD-2518K...	454	e-123
gi 12330738 emb AL157829.24 	Human DNA sequence from clone ...	454	e-123
gi 14270126 emb AL139385.12 	Human DNA sequence from clone ...	454	e-123
gi 19697556 gb AC002457.2 	Homo sapiens BAC clone CTB-60P12...	454	e-123
gi 21360122 gb AC026271.6 	Homo sapiens chromosome 17, clon...	454	e-123
gi 14572561 emb AL160275.14 	Human DNA sequence from clone ...	454	e-123

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|13270751|gb|AC013439.11|](#) **D** Homo sapiens BAC clone RP11-270G18 from 2, comple
Length = 167891

Score = 4556 bits (2369), Expect = 0.0
Identities = 2260/2411 (93%), Gaps = 3/2411 (0%)
Strand = Plus / Minus

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Query: 3955 agtctctctttgatgggtttgcacacttacctgcctctttcacctgcctctctagatatg 4014
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Sbjct: 129646 agtctctctttgatgggtttgcacacttacctgcctctttcacctgcctctctagatatg 129587

Query: 4015 aatgccacaatacgaaggattgaccagttaaccaacatcttagcccccatggctggttggc 4074
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Query: 7267 aagcaaatacatctgttggttgagacagtttaactgttgctatcctgttactagattata 7326
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|||||
Sbjct: 125712 aaattaactgattaatttcccttatgttgaggcatggaaaaaaa 125668

Score = 1829 bits (951), Expect = 0.0
Identities = 975/990 (98%), Gaps = 3/990 (0%)
Strand = Plus / Minus

Query: 1102 aagagtaattactgactttgaaagtctcataatgtagccaggccgtgcccttttgataag 1161
|||||
Sbjct: 139445 aagagtaattactgactttgaaagtctcataatgtagccaggaagtgcccttttgataag 139386

Query: 1162 gaagcaacttcttgagtacaatagactagaaacgaaaaatattccatcaaaacattttct 1221
|||||
Sbjct: 139385 gaagcaacttcttgagtacaatagactagaaacgaaaaatattccatcaaaacattttct 139326

Query: 1222 cttttcatttaagggagatcggatgtggcactttgcggtgtctgtgtttctggtagagct 1281
|||||
Sbjct: 139325 cttttcatttaagggagatcggatgtggcactttgcggtgtctgtgtttctggtagagct 139266

Query: 1282 ctatggaaacagcctccttttgacagcagctctacgggctggtggtggcagggctctgttct 1341
|||||
Sbjct: 139265 ctatggaaacagcctccttttgacagcagctctacgggctggtggtggcagggctctgttct 139206

Query: 1342 ggtcctgggagccatcatcgggtgactgggtggacaagaatgctagacttaaaggtgagtg 1401
|||||
Sbjct: 139205 ggtcctgggagccatcatcgggtgactgggtggacaagaatgctagacttaaaggtgagtg 139146

Query: 1402 ttgttatataattaagcccttttattcatgggaccaatgcctgagctacctctgtagcaa 1461
|||||
Sbjct: 139145 ttgttatataattaagcccttttattcatgggaccaatgcctgagctacctctgtagcaa 139086

Query: 1462 aggaaacaacaaactaggagagaaacaaccaggggaatgtctgcatgccacacttgaggga 1521
|||||
Sbjct: 139085 aggaaacaacaaactaggagagaaacaaccaggggaatgtctgcatgccacacttgaggga 139026

Query: 1522 ggagggdttagatggcaccacctctggatggaggggtcccatggctccacacaaagttgg 1581
|||||
Sbjct: 139025 ggagggcttagatggcaccacctctggatggaggggtcccatggctccacacaaagttgg 138966

Query: 1582 gatgcctggacattgacctaatagannnnnnngtatctttggctgttcataaatttcata 1641
|||||
Sbjct: 138965 gatgcctggacattgacctaatagattttttgtatctttggctgttcataaatttcata 138906

Query:	1642	tggttaatgattaaccttgtagcacttctctgagaacccatgttaaaccattaaaagtttgct	1701
Sbjct:	138905	tggttaatgattaaccttgtagcacttctctgagaacccatgttaaaccattaaaagtttgct	138846
Query:	1702	taactcaggcttctctaactgtatcttgtactggagtcctttagtgtgatgttcctgaga	1761
Sbjct:	138845	taactcaggcttctctaactgtatcttgtactggagtcctttagtgtgatgttcctgaga	138786
Query:	1762	cagctttaacatctgttctttggttactatgtttcatgtaagagtatgtataagggaatt	1821
Sbjct:	138785	cagctttaacatctgttctttggttactatgtttcatgtaagagtatgtataagggaatt	138726
Query:	1822	gaaaactaagaatagcttcaaggcagaatagttgagcctggatcacaaagagctgaatta	1881
Sbjct:	138725	gaaaactaagaatagcttcaaggcagaatagttgagcctggatcacaaagagctgaatta	138666
Query:	1882	taaattttgtagggaaaaagaagaaataataatatcttgatatttattctaagcattagt	1941
Sbjct:	138665	taaattttgtagggaaaaagaagaaataataatatcttgatatttattctaagcattagt	138606
Query:	1942	actgaaatcatgtcattttatacaggaaaagaaagtaattgatcaattaaattttccagt	2001
Sbjct:	138605	actgaaatcatgtcattttatacagg-aaagaaagtaattgatcaattaaattttccagt	138547
Query:	2002	atataagggaaatatggatgatcattcagggtaaattttcttgaattgctcaattgataa	2061
Sbjct:	138546	atataagggaaatatggatgatcattcagggtaaattttcttgaattgctcagttgataa	138487
Query:	2062	tggccaagaacctgaccatgcctgacttag	2091
Sbjct:	138486	t-gccaag-acctgaccatgcctgacttag	138459

Score = 1708 bits (888), Expect = 0.0
Identities = 890/907 (98%), Gaps = 2/907 (0%)
Strand = Plus / Minus

```
Query: 2979      gagggatgggggtgtggtataacccatgcatctggtgtcatattgaatcttcttgtgtata 3038
                |||
Sbjct: 136399   gagggatgggggtgtggtataaacccatgcatctggtgtcatattgaatcttcttgtgtata 136340

Query: 3039      tgtggattgatattatagagttgcaaagccaggtaggactttagaaatctttgagcctat 3098
                |||
Sbjct: 136339   tgtggattgatattatagagttgcaaagccaggtaggactttagaaatctttgagcctat 136280

Query: 3099      tcccttcattttattgaaaaaattaagacaaagtgaacgttagttgattgccattgtca 3158
                |||
```

Sbjct: 136279 tcccttcattttattgaaaaaattaagacaaagtgaacgtagttgattgccattgtca 136220

Query: 3159 tgcaactagaaggtgtcagaactctgacttaaatacaggtgttttcaattccccttcaac 3218
|||||

Sbjct: 136219 tgcaactagaaggtgtcagaactctgacttaaatacaggtgttttcaattccccttcaac 136160

Query: 3219 attcttttcaaaggcaatatttgtgggagaaatgttcaaaaccaccactgtgttaacatt 3278
|||||

Sbjct: 136159 attcttttcaaaggcaatatttgtgggagaaatgttcaaaaccaccactgtgttaacatt 136100

Query: 3279 ttataactgtattcacctgactattataattttgtattatgtgtactacagatgatcta 3338
|||||

Sbjct: 136099 ttataactgtattcacctgactattataattttgtattatgtgtactacagatgatcta 136040

Query: 3339 gatgatacaggttaggacattatgccattgactactggattcattcagtttcatatct 3398
|||||

Sbjct: 136039 gatgatacaggttaggacattatgccattgactactggattcattcagtttcatatct 135980

Query: 3399 ataacgtaaaatgatttcttataaatgaaattaaatacnnnnnnnatcattccaccaa 3458
|||||

Sbjct: 135979 ataacgtaaaatgatttcttataaatgaaattaaatactttttttatcattccaccaa 135920

Query: 3459 gactattttaactgccttgttttagtgacatatgtacagtgtggtaaactgacattataa 3518
|||||

Sbjct: 135919 gactattttaactgccttgttttagtgacatatgtacagtgtggtaaactgacattataa 135860

Query: 3519 ctcannnnnncttgtcattcttttagacttctgctatatcctgatcatcactattgcaa 3578
|||||

Sbjct: 135859 ctcatTTTTTTTcttgtcattcttttagacttctgctatatcctgatcatcactattgcaa 135800

Query: 3579 atattgcaaatttggccagtagtactgctactgcaatcacaatccaaagggattggattgttg 3638
|||||

Sbjct: 135799 atattgcaaatttggccagtagtactgctactgcaatcacaatccaaagggattggattgttg 135740

Query: 3639 ttgttgcaggagaagacagaagcaaactagcaagtaatttggctttctcttttaataa 3698
|||||

Sbjct: 135739 ttgttgcaggagaagacagaagcaaactagcaagtaatttggctttctcttttaataa 135680

Query: 3699 tgagcatgttaggattcactttaaatcggtggtgataaatgaggctgtaag-cttgtatt 3757
|||||

Sbjct: 135679 tgagcatgttaggattcactttaaatcggtggtgataaatgaggctgtaagccttgtatt 135620

Query: 3758 tttgttctgggtattttttaagaatgataaattgaaagcatac-ttttttcttaccttat 3816
|||||

Sbjct: 135619 tttgttctgggtattttttaagaatgataaattgaaagcatacttttttcttaccttat 135560

Query: 3817 tgtcagtttttagtgctgatttatctcactgttacgaagttaacttataggatagctaact 3876
|||||

Sbjct: 135559 tgtcagtttttagtgctgatttatctcactgttacgaagttaacttataggatagctaact 135500

Query: 3877 tctcttt 3883

|||||

Sbjct: 135499 tctcttt 135493

Score = 1504 bits (782), Expect = 0.0

Identities = 834/865 (96%), Gaps = 4/865 (0%)

Strand = Plus / Minus

Query: 2114 atcatctgc-tactgag-ggcagagaaaaggctaccagggtgtctttatctgtccttactc 2171

||||||| ||||| |||||||||||||||||||||||||||||||||||

Sbjct: 137614 atcatctgcctactgagtggcagagaaaaggctaccagggtgtctttatctgtccttactc 137555

Query: 2172 cagtgccttatctatatgggcgcctcataagagagttgccatctgtgatgaaagggg-ag 2230

||||||||||||||||||||||||||||||||| ||||||||||| ||||| ||

Sbjct: 137554 cagtgccttatctatatgggcgcctcataagagaattgccatctgtgatggaaggggtag 137495

Query: 2231 cttagaatttcgtagcaatggcaaatagcgttagtatgcaaagaaataccctgctgcttt 2290

||||||||||||||||||||||||||||||||| ||||||||||| |||||||

Sbjct: 137494 cttagaatttcgtagcaatggcaaatagcatttagtatgcaaagaaatacactgctgcttt 137435

Query: 2291 attctgggcaaatttttgtgtgtcttttctatttaggtaagccatattatcagattcagc 2350

||||| ||||||||||||||||||||||||||||||| |||||||||||

Sbjct: 137434 attcttggcaaatttttgtgtgtcttttctatttaggtaaaccatattatcagattcagc 137375

Query: 2351 ctgccatgtaggaggttgtaggttgataacttcctctttaacctcatacatgttattgt 2410

||||||||| ||||| || |||||||||||||||||||||||||||||||

Sbjct: 137374 ctgccatgtaggaggttgtagatttcataacttcctctttaacctcatacatgttattgt 137315

Query: 2411 tttaccttaagcaacaaagagctgaaatgtggatcatgtctatatcatactacagctcca 2470

||||||||| |||||||||||||||||||||||||||||||

Sbjct: 137314 tttaccttaagcaacaaagagctgaaatgtggatcatgtctatatcatactacagctcca 137255

Query: 2471 tttatgttaaactttcaagaagataaaactaaatgaaaaggtagtcattatgatagacttc 2530

||||||||| |||||||||||||||||||||||||||||||

Sbjct: 137254 tttatgttaaactttcaagaagataaaactaaatgaaaatgtagtcattatgatagacttc 137195

Query: 2531 agtgagcagagaagcttgtggtacttcatcatttggttgcatacttactggctggtgt 2590

||||| ||||| |||||||||||||||||||||||

Sbjct: 137194 agtgaacagagaaacttgtggtacttcatcatttggttgcatacttactggctggtgt 137135

Query: 2591 gatcctctgggttgattgagagtagttgaggcaggac-gacttcagaaagggtttcttt 2649

||||||||| ||||||||||||||||||||||| |||||||

Sbjct: 137134 gatcctctgggttgattgagagtagttgaggcaggactgacttcagaaagggtttcttt 137075

Query: 2650 ttatctggtaataattaggtctgggtattaatgtattatagtagagcaattatgtgtgga 2709

|||||
Sbjct: 137074 ttatctggttaataattaggtctgtgtattaatgtattatagtagaacaattatgtgtgga 137015

Query: 2710 taagagcagtcctcagtgagccatTTTgatgtaatgtacactTTTctctcttctcctctgcaca 2769
|||||
Sbjct: 137014 taagaacagtcctcactgagacatTTTgatgtaatgtacactTTTctctcttctcctctgcaca 136955

Query: 2770 gtggccagacctcgctggtggtacagaatgTTTcagtcacctgtgtggaatcatcctg 2829
|||||
Sbjct: 136954 gtggccagacctcgctggtggtacagaatgTTTcagtcacctgtgtggaatcatcctg 136895

Query: 2830 atgatggTTTTcttacataaacatgagcttctgaccatgtaccatggatgggTTTctcgta 2889
|||||
Sbjct: 136894 atgatggTTTTcttacataaacatgagcttctgaccatgtaccatggatgggTTTctcgta 136835

Query: 2890 agttctcaatgagattcttgatggcagaaaattgaatatctggtagtggttaaaggatgaa 2949
|||||
Sbjct: 136834 agttctcaatgagattcttgatggcagaaaattgaatatctggtagtggttaaaggatgaa 136775

Query: 2950 aatgctTTTgaagctannnnnnnnnn 2974
|||||
Sbjct: 136774 aatgctTTTgaagctatTTTTTTTTT 136750

Score = 1143 bits (594), Expect = 0.0
Identities = 579/611 (94%), Gaps = 1/611 (0%)
Strand = Plus / Minus

Query: 1 agctggctcagggcgctccgctaggctcggacgacctgctgagcctcccaaaccgcttcca 60
|||||
Sbjct: 144757 agctggctcagggcgctccgctaggctcggacgacctgctgagcctcccaaaccgcttcca 144698

Query: 61 taaggctTTTgc-TTTccaacttcagctacagtgttagctaagTTTggaaagaaggaaaaa 119
|||||
Sbjct: 144697 taaggctTTTgcTTTccaacttcagctacagtgttagctaagTTTggaaagaaggaaaaa 144638

Query: 120 agaaaatccctgggccccTTTTctTTTgttctTTTgcaaagtcgctcgttgtagtctTTTT 179
|||||
Sbjct: 144637 agaaaatccctgggccccTTTTctTTTgttctTTTgcaaagtcgctcgttgtagtctTTTT 144578

Query: 180 gcccaaggctgttggtgtTTTtagaggtgctatctccagttccttgcaactcctgttaacaa 239
|||||
Sbjct: 144577 gcccaaggctgttggtgtTTTtagaggtgctatctccagttccttgcaactcctgttaacaa 144518

Query: 240 gcacctcagcgagagcagcagcagcgatagcagccgcagaagagccagcggggTgccta 299
|||||
Sbjct: 144517 gcacctcagcgagagcagcagcagcgatagcagccgcagaagagccagcggggTgccta 144458

Query: 920 cttggccgactacctgacctctgcaaaattccttctctaccttggtcattctctctctac 979
|||||
Sbjct: 143868 cttggccgactacctgacctctgcaaaattccttctctaccttggtcattctctctctac 143809

Query: 980 ttgggtaagtgagaatgcatagtcttacaacacagttgcgcaattttttatttcctttcg 1039
|||||

Sbjct: 143808 ttgggtaagtgagaatgcatagtcttacaacacagttgcgcaattttttatttcctttcg 143749

```
Query: 1040      ttctagccagttgtattaaagccaacttccagttttgtcaagcagttaaagaaataaa 1096
                |||
Sbjct: 143748    ttctagccagttgtattaaagccaacttccagttttgtcaagcagttaaagaaataaa 143692
```

Score = 410 bits (213), Expect = e-110
Identities = 256/297 (86%)
Strand = Plus / Minus

Query: 4753 nnnnnnnnnnnnnngagacagagtctcgctctgttgcccaggctgaagtgcagtgccgcg 4812
 ||||| ||| | || ||||| ||| || | ||||| ||
 Sbjct: 103977 ttttttttttttttgagacggagtttgcactgttgccagactggagtgcagtgccacg 103918

Query: 4813 atcttggtcactgcaagctctgctcctgggttcacgccatttctctgcctcagcctcc 4872
 |||
 Sbjct: 103917 atcttggtcactgcaagctctgctccgggttcacaccatttctctgcctcagcctcc 103858

```
Query: 4873      caagtagctgggattgcaggcatccaccaccaccccggttaatTTTTTgtatttttagt 4932
                ||| ||||| | | ||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 103857    caagtagcttgaactacaggggccaccaccacgcccgggttaatTTTTTgtacttttagt 103798
```

Query: 4933 agagacggggtttcaccatgtagccaggatggtcttgatctcctgacctcgtgatctgc 4992
 |||||
 Sbjct: 103797 agagacagggtttcaccatgtagtcaggatggtcttgatctcctgacctcgtgatctgc 103738

```
Query: 4993      ccgcctcggcctcccaaagtctgggattacaggtgtgagccacgtgcttggccaa 5049
                ||||| |||||||||||||||| ||||||| ||||||||| |||||||||
Sbjct: 103737   ccgccttggcctcccaaagtctgagattacaggcgtgagccaccactccttggccaa 103681
```

Score = 352 bits (183), Expect = 6e-93
Identities = 251/302 (83%), Gaps = 12/302 (3%)
Strand = Plus / Plus

Query: 4753 nnnnnnnnnnnnngagacagagtctcgctctgttgcccaggctgaagtgcagtgggcgcg 4812
||||| |||||
Sbjct: 151136 tttttttttttttagatggagtcctcgctctgttgcccaggctggagtgcaagtggcacg 151195

Query: 4813 atcttggctcactgcaagctctgcctcctgggttcacgccattctcctgcctcagcctcc 4872